STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____ 10/551,300
Source: _____ IFWP
Date Processed by STIC: _____ 06/20/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/551,300_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
   Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino
   Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
   "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
   (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
   (NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
   (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or **Xaa** represents.

10____Invalid <213>
   Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220>

~~Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0
   "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/551,300

DATE: 06/20/2006
TIME: 12:03:24

Input Set : **E:\SEQLIST.TXT**
Output Set: **N:\CRF4\06202006\J551300.raw**

```
 4 <110> APPLICANT: Trotta, Christopher R.
 6 <120> TITLE OF INVENTION: TARGETING ENZYMES OF THE tRNA SPLICING
 7       PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR
 8       ANTI-PROLIFERATIVE MOLECULES
10 <130> FILE REFERENCE: 10589-034-999
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/551,300
C--> 13 <141> CURRENT FILING DATE: 2005-09-27
15 <150> PRIOR APPLICATION NUMBER: PCT/US2004/009590
16 <151> PRIOR FILING DATE: 2004-03-26
18 <150> PRIOR APPLICATION NUMBER: 60/458,067
19 <151> PRIOR FILING DATE: 2003-03-27
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 465
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <223> OTHER INFORMATION: HsSen2p
33 <400> SEQUENCE: 1
34 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
35 1               5                   10                  15
36 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
37             20                  25                  30
38 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
39         35                  40                  45
40 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
41     50                  55                  60
42 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
43 65                  70                  75                  80
44 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
45              85                  90                  95
46 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
47             100                 105                 110
48 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
49         115                 120                 125
50 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
51     130                 135                 140
52 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
53 145                 150                 155                 160
54 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
55              165                 170                 175
56 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
```

```
57              180                185                190
58 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
59              195                200                205
60 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
61       210                215                220
62 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
63 225                230                235                240
64 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
65              245                250                255
66 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
67              260                265                270
68 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
69       275                280                285
70 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala
71       290                295                300
72 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys
73 305                310                315                320
74 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln
75              325                330                335
76 Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys
77       340                345                350
78 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu
79              355                360                365
80 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile
81       370                375                380
82 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser
83 385                390                395                400
84 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys
85              405                410                415
86 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys
87              420                425                430
88 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val
89       435                440                445
90 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp
91       450                455                460
92 Leu
93 465
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 448
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <223> OTHER INFORMATION: HsSen2 variant
104 <400> SEQUENCE: 2
105 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
106 1               5                  10                 15
107 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
108              20                 25                 30
109 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
```

```
110          35                 40                 45
111 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
112     50                 55                 60
113 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
114 65                 70                 75                 80
115 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
116             85                 90                 95
117 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
118             100                105                110
119 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
120         115                120                125
121 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
122     130                135                140
123 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
124 145                150                155                160
125 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
126             165                170                175
127 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
128             180                185                190
129 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
130         195                200                205
131 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
132     210                215                220
133 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
134 225                230                235                240
135 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
136             245                250                255
137 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
138             260                265                270
139 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
140         275                280                285
141 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Glu
142     290                295                300
143 Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln Pro
144 305                310                315                320
145 Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys Gly
146             325                330                335
147 Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu Tyr
148             340                345                350
149 Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile Glu
150         355                360                365
151 Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser Trp
152     370                375                380
153 Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys Glu
154 385                390                395                400
155 Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys Glu
156             405                410                415
157 Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val Ile
158             420                425                430
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RAW SEQUENCE LISTING   DATE: 06/20/2006
PATENT APPLICATION: US/10/551,300   TIME: 12:03:24

Input Set : E:\SEQLIST.TXT
Output Set: N:\CRF4\06202006\J551300.raw

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163 <210> SEQ ID NO: 3
164 <211> LENGTH: 377
165 <212> TYPE: PRT
166 <213> ORGANISM: Saccharomyces cerevisiae
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Sc Sen2p
171 <400> SEQUENCE: 3
172 Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro
173 1               5               10              15
174 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
175             20              25              30
176 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
177         35              40              45
178 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile
179     50              55              60
180 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
181 65              70              75              80
182 Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg
183             85              90              95
184 Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly
185             100             105             110
186 Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr
187         115             120             125
188 Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys
189     130             135             140
190 Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp
191 145             150             155             160
192 Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe
193             165             170             175
194 Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp
195             180             185             190
196 Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu
197         195             200             205
198 Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu
199     210             215             220
200 Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala
201 225             230             235             240
202 Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile
203             245             250             255
204 His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
205             260             265             270
206 Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
207         275             280             285
208 Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly
209     290             295             300
210 Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
211 305             310             315             320
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RAW SEQUENCE LISTING   DATE: 06/20/2006
PATENT APPLICATION: **US/10/551,300** TIME: 12:03:24

Input Set : **E:\SEQLIST.TXT**
Output Set: **N:\CRF4\06202006\J551300.raw**

```
212 Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu
213             325             330             335
214 Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn
215             340             345             ·350
216 Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys
217         355             360             365
218 Arg Trp Val Pro Gly Arg Asn Arg Asp
219     370             375
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 5
224 <212> TYPE: PRT
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Motif
230 <400> SEQUENCE: 4
231 Tyr Arg Gly Gly Tyr
232 1               5
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Invalid Response.
What is the Source
of genetic Material?
Pls See Item # 11
on Error Summary

VERIFICATION SUMMARY   DATE: 06/20/2006
PATENT APPLICATION: **US/10/551,300**   TIME: 12:03:25

Input Set : **E:\SEQLIST.TXT**
Output Set: **N:\CRF4\06202006\J551300.raw**

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date